Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:08:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080812.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3080812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080812.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:08:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,688,996
Mapped reads	2,167,609 / 80.61%
Unmapped reads	521,387 / 19.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,246 / 0.9%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	178,796 / 6.65%
Duplication rate	6.93%
Clipped reads	861,955 / 32.05%

2.2. ACGT Content

Number/percentage of A's	43,053,287 / 29.15%
Number/percentage of C's	27,188,029 / 18.41%
Number/percentage of T's	46,114,243 / 31.22%
Number/percentage of G's	31,336,814 / 21.21%
Number/percentage of N's	20,035 / 0.01%
GC Percentage	39.62%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.3941

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

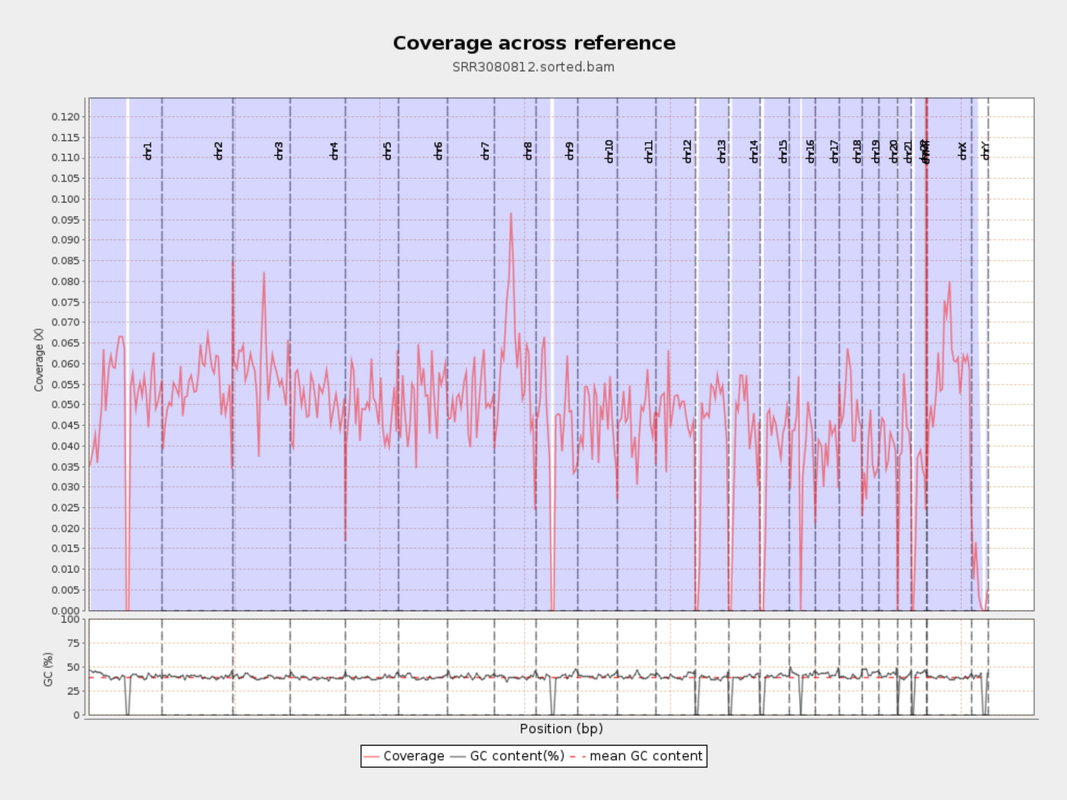
General error rate	0.8%
Mismatches	1,167,798
Insertions	11,019
Mapped reads with at least one insertion	0.5%
Deletions	30,313
Mapped reads with at least one deletion	1.38%
Homopolymer indels	47.92%

2.6. Chromosome stats

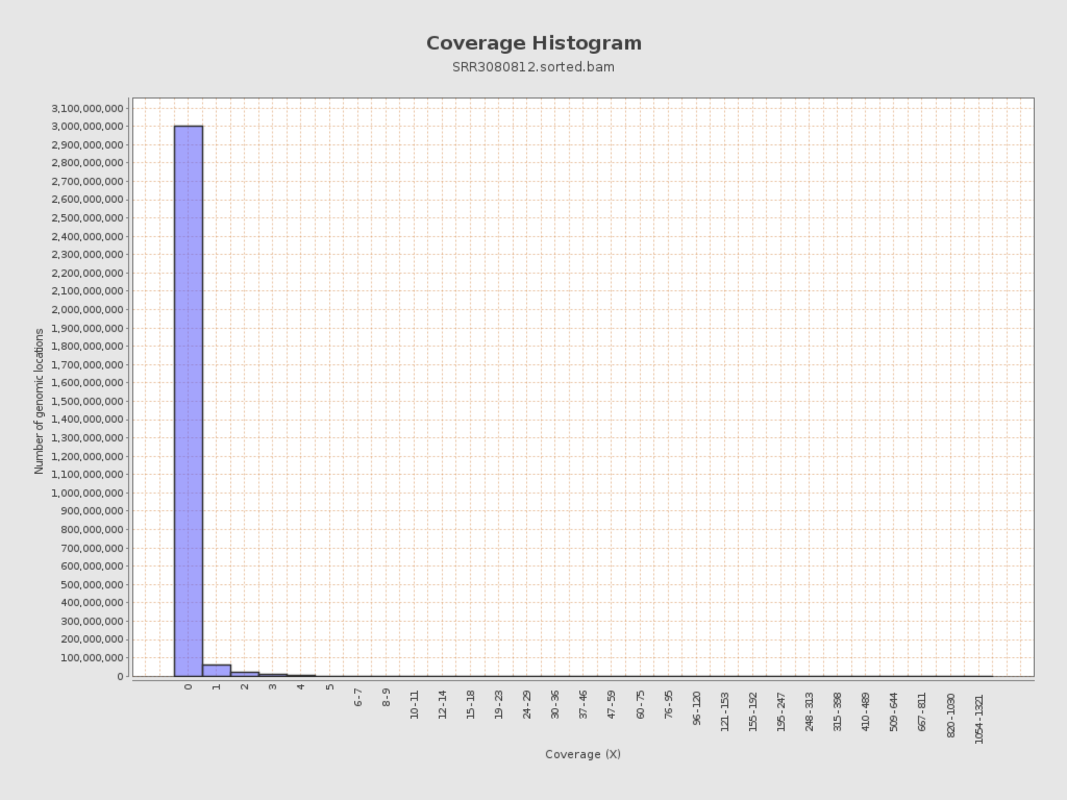
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12527069	0.0503	0.4417
chr2	243199373	13196323	0.0543	0.4292
chr3	198022430	11729452	0.0592	0.3548
chr4	191154276	9757748	0.051	0.3344
chr5	180915260	8880574	0.0491	0.3207
chr6	171115067	8833379	0.0516	0.3465
chr7	159138663	8176609	0.0514	0.3999

chr8	146364022	8853066	0.0605	0.8715
chr9	141213431	6079232	0.043	0.3399
chr10	135534747	6325867	0.0467	0.3515
chr11	135006516	6210540	0.046	0.3281
chr12	133851895	6471079	0.0483	0.319
chr13	115169878	4830131	0.0419	0.3024
chr14	107349540	4254497	0.0396	0.2961
chr15	102531392	3710344	0.0362	0.2783
chr16	90354753	3536102	0.0391	0.29
chr17	81195210	3130225	0.0386	0.2841
chr18	78077248	3894162	0.0499	0.4913
chr19	59128983	2108760	0.0357	0.328
chr20	63025520	2544289	0.0404	0.293
chr21	48129895	1896436	0.0394	0.299
chr22	51304566	1270307	0.0248	0.2235
chrMT	16571	214677	12.955	7.925
chrX	155270560	9001508	0.058	0.3551
chrY	59373566	333031	0.0056	0.1248

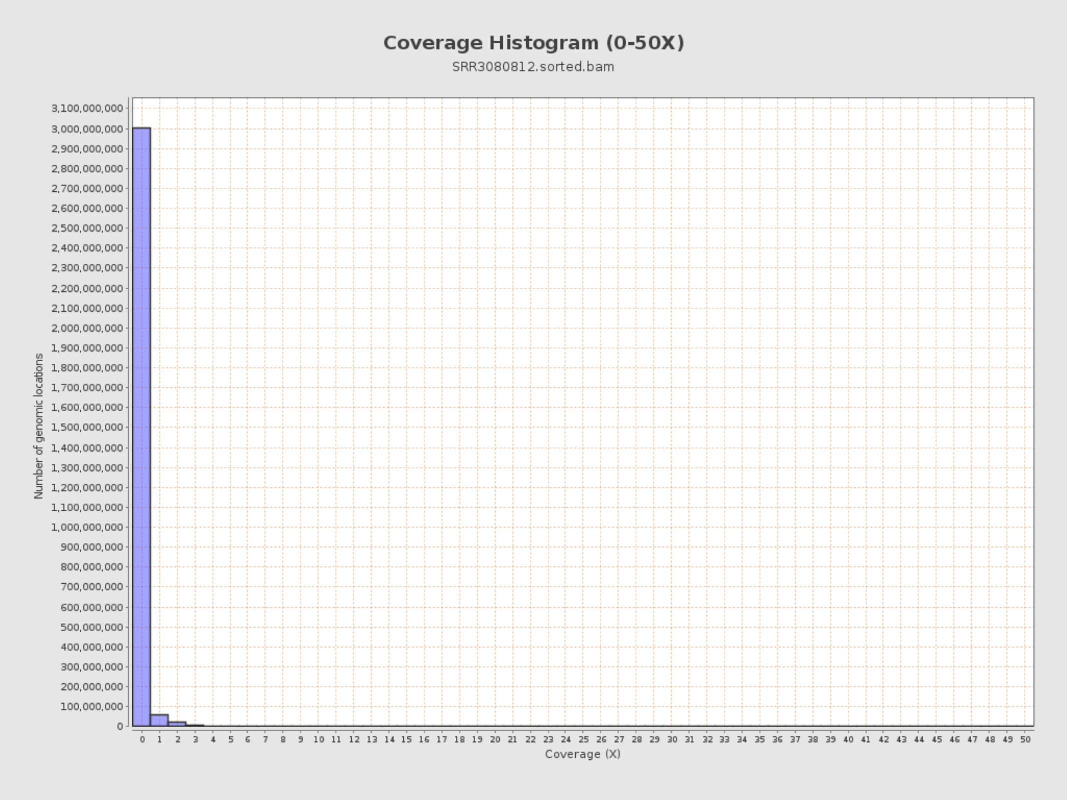
3. Results : Coverage across reference



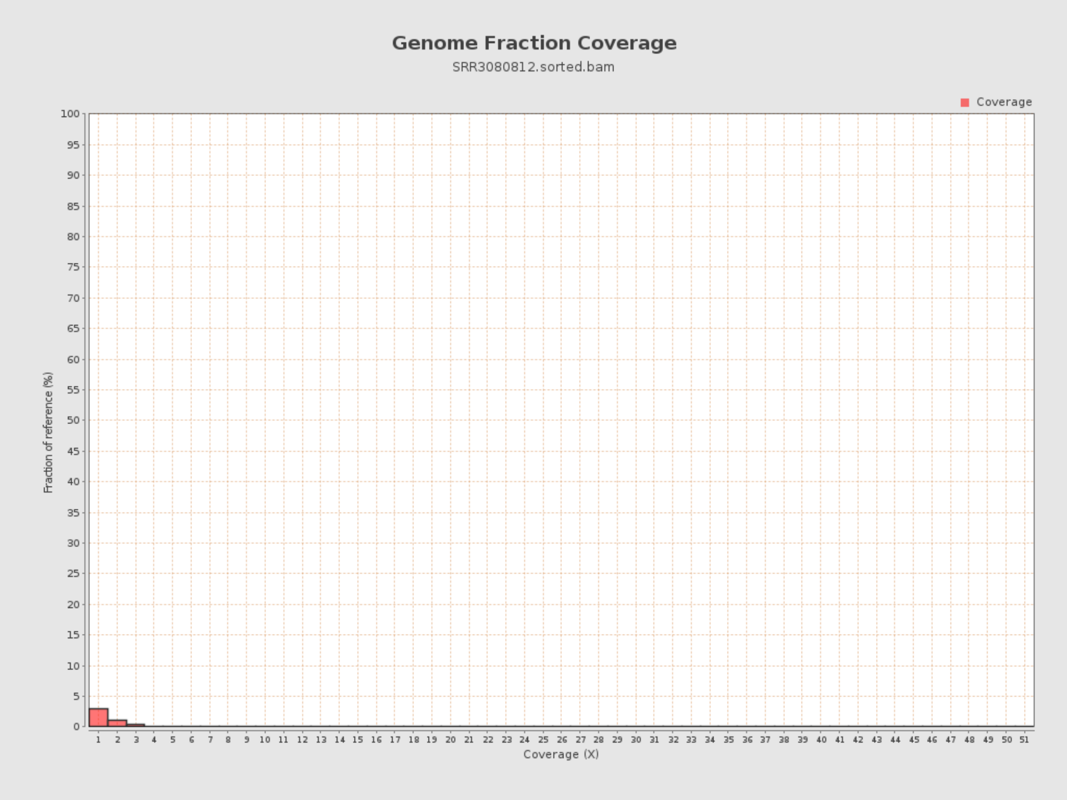
4. Results : Coverage Histogram



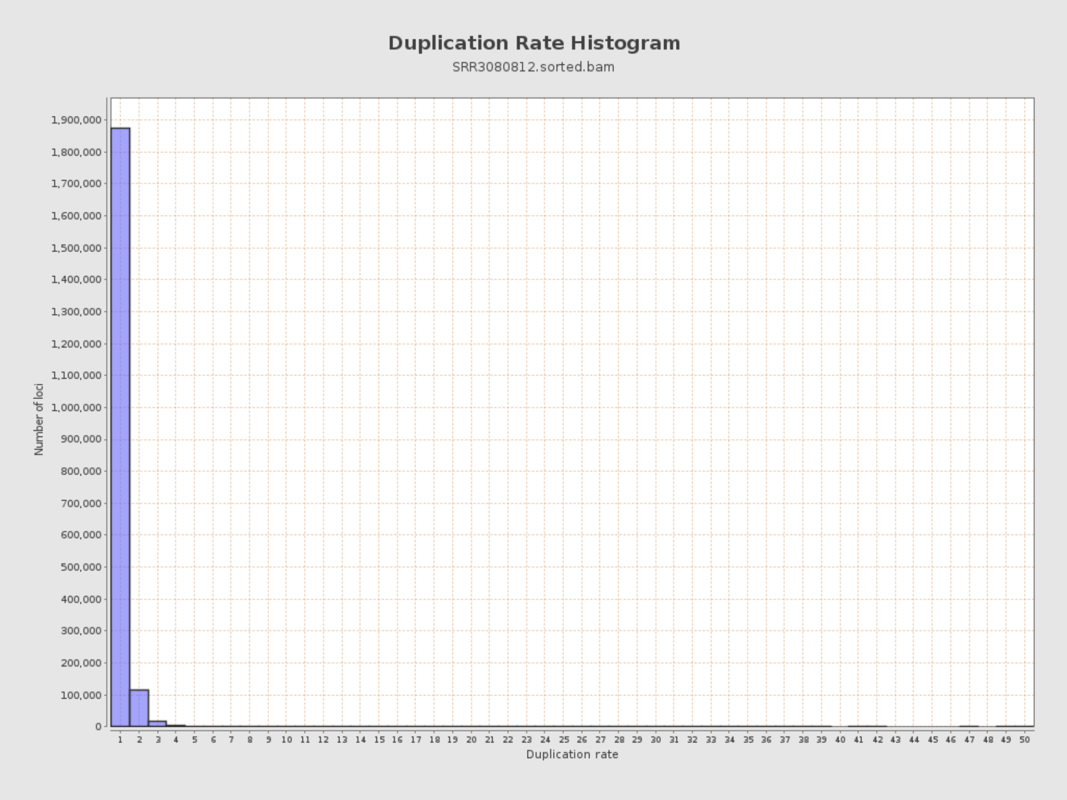
5. Results : Coverage Histogram (0-50X)



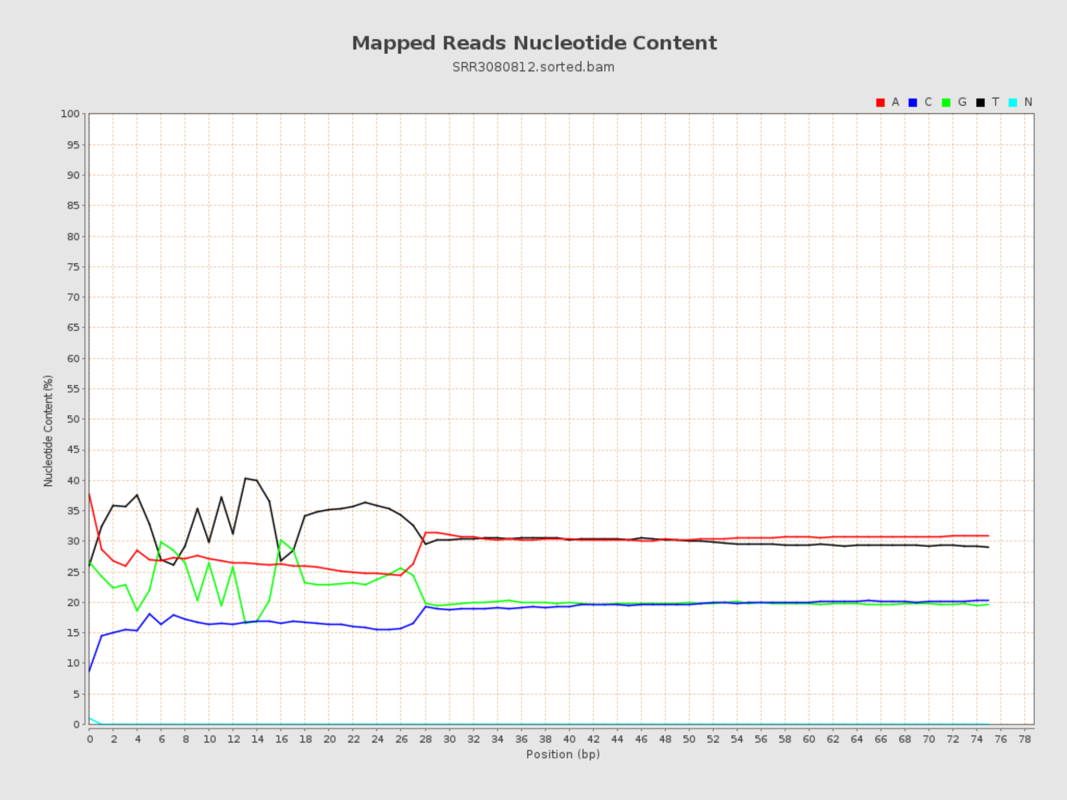
6. Results : Genome Fraction Coverage



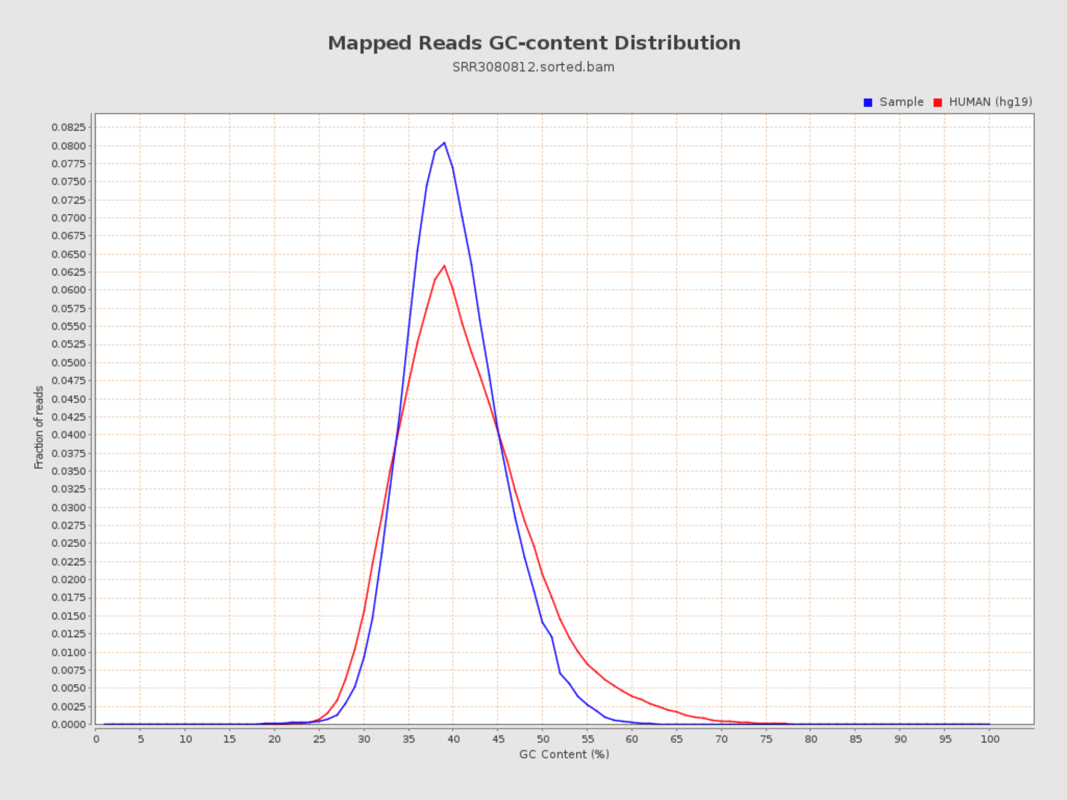
7. Results : Duplication Rate Histogram



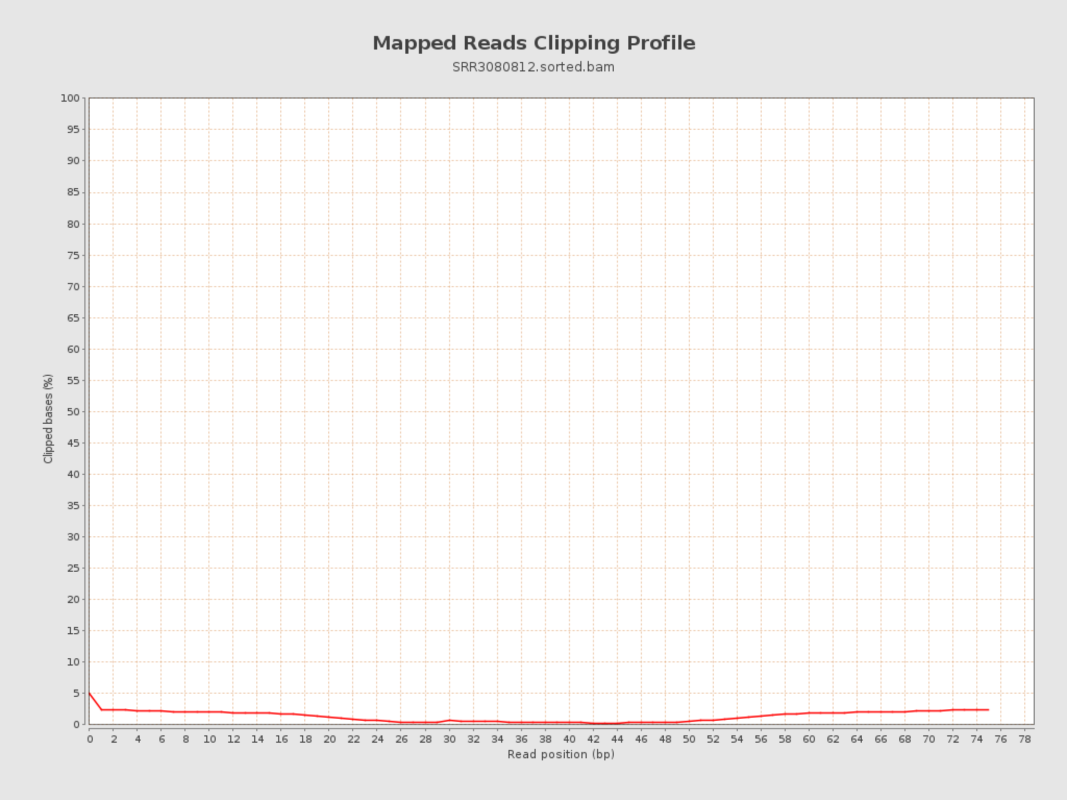
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



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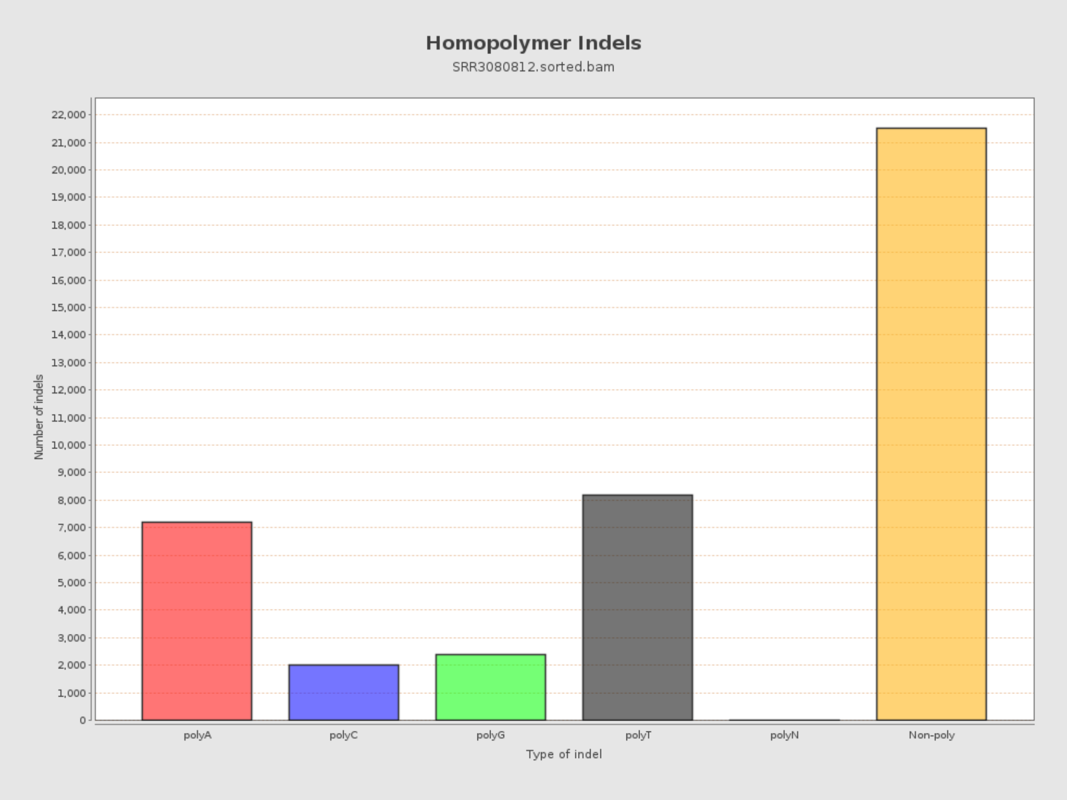
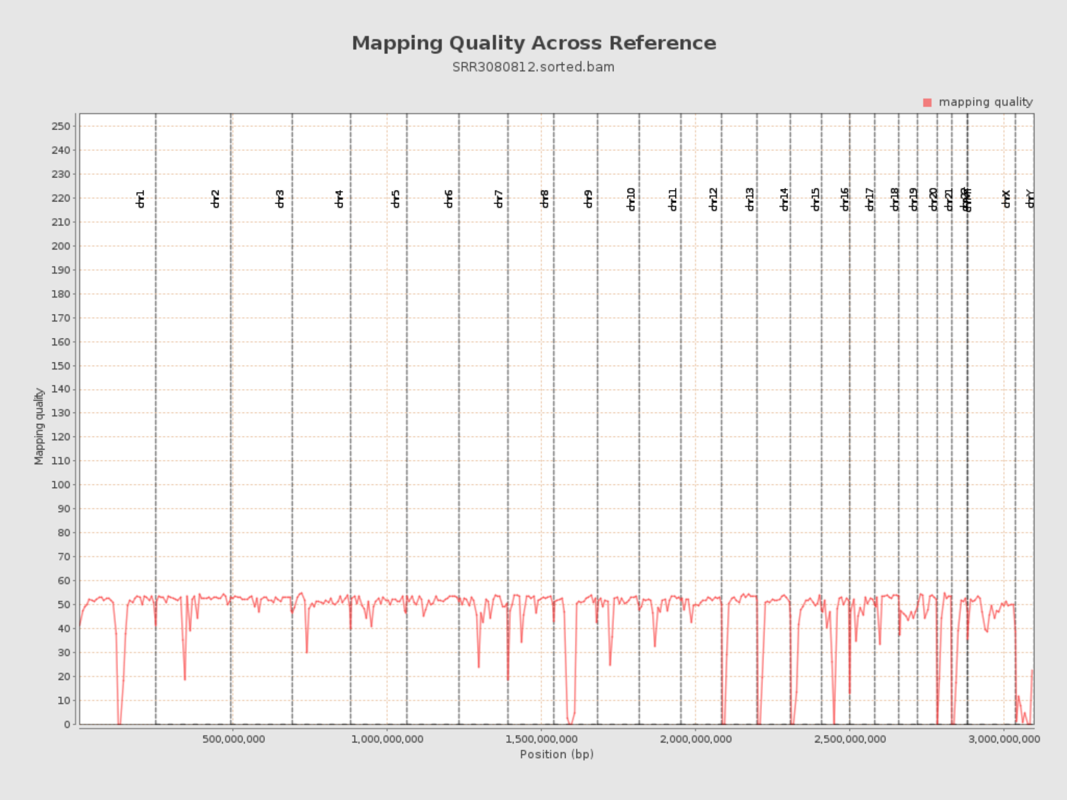
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram